METHOD AND APPARATUS FOR EXTRACTING AND EVALUATING MUTUALLY SIMILAR PORTIONS IN ONE-DIMENSIONAL SEQUENCES IN MOLECULES AND/OR THREE-DIMENSIONAL STRUCTURES OF MOLECULES

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ABSTRACT OF THE DISCLOSURE

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In the analysis of one-dimensional sequences of molecules, the longest common subsequence, the number of elements constituting the subsequence, and appearance positions of the subsequence are determined by a novel and simple method, and processes, such as
15 homology decision, homology search, motif search and alignment are performed based on the results. In the analysis of these-dimensional structures of molecules, limiting conditions, such as geometrical arrangements of elements, are introduced to realize the
20 determination of correspondence of three-dimensional structures at high speeds, and whereby it is made possible to achieve such processing as superposed display of three-dimensional structure of molecules, retrieval of three-dimensional structure, and
25 evaluation of functions. Moreover, the molecules are divided into secondary structure that are then related to each other based on spatial similarity among the secondary structures. Furthermore, similarity among
30 the molecules is decided based on a relationship of spatial positions of the corresponding secondary structures.